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## ANALYSIS TOOLS

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## Generic DB Entry Retrieval

```

ID      HSM017132  standard; RNA; EST; 507 BP.
XX
AC      AL121363;
XX
EV      AL121363.1
XX
DT      25-SEP-1999 (Rel. 61, Created)
DT      26-FEB-2000 (Rel. 62, Last updated, Version 2)
XX
DE      Homo sapiens mRNA; EST DKFZp762C027_r1 (from clone DKFZp762C027)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN      [1]
RP      1-507
RA      Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RT      ;
FL      Submitted (18-FEB-2000) to the EMBL/GenBank/DDBJ databases.
FL      MIPS, Am Klopferspitz 18a, D-32152 Martinsried, GERMANY
XX
RF      RZPD; DKFZp762C027; DKFZp762C027.
DE      UNILIB; 2390; 2393.
XX
CC      This is the 5' sequence of the clone insert
CC      Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC      Research Center (DKFZ) ; Email: s.wiemann@dkfz-heidelberg.de;
CC      sequenced by MediGenomix, Martinsried, Germany, within the cDNA
CC      sequencing consortium of the German Genome Project.
CC      cDNA sequence also available.
CC      This clone (DKFZp762C027) is available at the RZPD in Berlin.
CC      Please contact the RZPD: Reinspurcentrum, Heubnerweg 6,
CC      14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key          Location/Qualifiers
FH
FT      exon          1..507
FT      cds          1..507
FT      ORF          1..507

```

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FT      <dev_stage="adult">
FT      /tissue_type="melanoma (MeWo cell line)"
XX
SQ      Sequence 507 BP; 117 A; 152 C; 151 G; 87 T; 0 other;
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      aacggggggt ttatgagga cgtgtgtgag tatgaaggca tcttggatgc aagcaaaacag      12
      cggcacaaca agctgtggcg tcagcagaca gacagcagcc tcacgcagcc tgtggatgac      18
      cctgcaggac ctggcgactt cttgcagag agcccagatg gcaccccgga aagccagctg      24
      cctctcttgg atgatgcgc ccagcccggc ttaggggccc ccttccctg ctgtttccgg      30
      cgaactctcag acccccttct gccttccctt gaggatgaaa ctggcagctt ggtccacctg      36
      gaggatccgg agagggaggg tctgttggag gaagctgctc cactgcaga ggtgcacagg      42
      ccggccagac agccccagca aggttccgga ctctgtgaga aggatgtgaa gaagaaaacta      48
      gactttggga gtcccaaaagg tcggagc                                50
```

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